RAW SEQUENCE LISTING
PATENT APPLICATION **US/09/351,149**

DATE: 07/28/1999
TIME: 15:00:19

Input Set: **I351149.RAW**

This Raw Listing contains the General Information Section and up to first 5 pages.

ENTERED

<110> APPLICANT: THORPE, PHILIP E.
RAN, SOPHIA
<120> TITLE OF INVENTION: CANCER TREATMENT KITS COMPRISING THERAPEUTIC CONJUGATES THAT BIND TO AMINOPHOSPHOLIPIDS
<130> FILE REFERENCE: 4001.002383
<140> CURRENT APPLICATION NUMBER: US/09/351,149
<141> CURRENT FILING DATE: 1999-07-12
<160> NUMBER OF SEQ ID NOS: 5
<170> SOFTWARE: PatentIn Ver. 2.0
<210> SEQ ID NO 1
<211> LENGTH: 2149
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

cagctgactc aggcaggctc catgctgaac ggtcacacag agaggaaaca ataaatctca 60
gctactatgc aataaatatc tcaagtttta acgaagaaaa acatcattgc agtgaaataa 120
aaaattttaa aattttagaa caaagctaac aaatggctag ttttctatga ttcttcttca 180
aacgctttct ttgaggggga aagagtcaaa caaacaagca gttttacctg aaataaagaa 240
ctagttttag aggtcagaag aaaggagcaa gttttgcgag aggcacggaa ggagtgtgct 300
ggcagtacaa tgacagtttt cctttccttt gctttcctcg ctgccattct gactcacata 360
gggtgcagca atcagcgccg aagtccagaa aacagtggga gaagatataa ccggattcaa 420
catgggcaat gtgcctacac tttcattctt ccagaacacg atggcaactg tcgtgagagt 480
acgacagacc agtacaacac aaacgctctg cagagagatg ctccacacgt ggaaccggat 540
ttctcttccc agaaacttca acatctggaa catgtgatgg aaaattatac tcagtggctg 600
caaaaacttg agaattacat tgtggaaaac atgaagtcgg agatggccca gatacagcag 660
aatgcagttc agaaccacac ggctaccatg ctggagatag gaaccagcct cctctctcag 720
actgcagagc agaccagaaa gctgacagat gttgagaccc aggtactaaa tcaaacttct 780
cgacttgaga tacagctgct ggagaattca ttatccacct acaagctaga gaagcaactt 840
cttcaacaga caaatgaaat cttgaagatc catgaaaaaa acagtttatt agaacataaa 900
atcttagaaa tggaaggaaa acacaaggaa gagttggaca ccttaaagga agagaaagag 960
aaccttcaag gcttggttac tcgtcaaaca tatataatcc aggagctgga aaagcaatta 1020
aacagagcta ccaccaacaa cagtgtcctt cagaagcagc aactggagct gatggacaca 1080
gtccacaacc ttgtcaatct ttgcactaaa gaaggtgttt tactaaaggg aggaaaaaga 1140
gaggaagaga aaccatttag agactgtgca gatgtatatc aagctggttt taataaaagt 1200
ggaatctaca ctatttatat taataatatg ccagaaccca aaaaggtgtt ttgcaatatg 1260
gatgtcaatg ggggaggttg gactgtaata caacatcgtg aagatggaag tctagatttc 1320
caaagaggct ggaaggaata taaaatgggt tttggaaatc cctccggtga atattggctg 1380
gggaatgagt ttatttttgc cattaccagt cagaggcagt acatgctaag aattgagtta 1440
atggactggg aagggaaccg agcctattca cagtatgaca gattccacat aggaaatgaa 1500
aagcaaaact ataggttgta tttaaaaggt cacactggga cagcaggaaa acagagcagc 1560
ctgatcttac acggtgctga tttcagcact aaagatgctg ataatgacaa ctgtatgtgc 1620
aaatgtgccc tcatgttaac aggaggatgg tggtttgatg cttgtggccc ctccaatcta 1680
aatggaatgt tctatactgc gggacaaaac catggaaaac tgaatgggat aaagtggcac 1740
tacttcaaag ggcccagtta ctccttacgt tccacaacta tgatgattcg acctttagat 1800

ttttgaaagc gcaatgtcag aagcgattat gaaagcaaca aagaaatccg gagaagctgc 1860
caggtgagaa actgtttgaa aacttcagaa gcaaacaata ttgtctccct tccagcaata 1920
agtggtagtt atgtgaagtc accaaggttc ttgaccgtga atctggagcc gtttgagttc 1980
acaagagtct ctacttgggg tgacagtgct cacgtggctc gactatagaa aactccactg 2040
actgtcgggc tttaaaaagg gaagaaactg ctgagcttgc tgtgcttcaa actactactg 2100
gaccttattt tggaactatg gtagccagat gataaatatg gttaatttc 2149

<210> SEQ ID NO 2
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2

Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
1 5 10 15
Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
20 25 30
Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
35 40 45
Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
50 55 60
Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
65 70 75 80
Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
85 90 95
Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
100 105 110
Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
115 120 125
Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
130 135 140
Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
145 150 155 160
Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
165 170 175
Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
180 185 190
Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
195 200 205
Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
210 215 220
Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
225 230 235 240
Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
245 250 255
Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
260 265 270
Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
275 280 285
Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
290 295 300
Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn

```
95          305                 310                 315                 320
96          Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
97                          325                 330                 335
98          Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
99                      340                 345                 350
100         Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
101                 355                 360                 365
102         Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
103             370                 375                 380
104         Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
105         385                 390                 395                 400
106         Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
107                         405                 410                 415
108         Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
109                     420                 425                 430
110         Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
111                 435                 440                 445
112         Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
113             450                 455                 460
114         Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
115         465                 470                 475                 480
116         Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu
117                         485                 490                 495
118         Asp Phe
119     <210> SEQ ID NO 3
120     <211> LENGTH: 2269
121     <212> TYPE: DNA
122     <213> ORGANISM: Homo sapiens
123     <400> SEQUENCE: 3
124         tgggttggtg tttatctcct cccagccttg agggagggaa caacactgta ggatctgggg 60
125         agagaggaac aaaggaccgt gaaagctgct ctgtaaaagc tgacacagcc ctcccaagtg 120
126         agcaggactg ttcttcccac tgcaatctga cagtttactg catgcctgga gagaacacag 180
127         cagtaaaaac caggtttgct actggaaaaa gaggaaagag aagactttca ttgacggacc 240
128         cagccatggc agcgtagcag ccctgcgttt cagacggcag cagctcggga ctctggacgt 300
129         gtgtttgccc tcaagtttgc taagctgctg gtttattact gaagaaagaa tgtggcagat 360
130         tgttttcttt actctgagct gtgatcttgt cttggccgca gcctataaca actttcggaa 420
131         gagcatggac agcataggaa agaagcaata tcaggtccag catgggtcct gcagctacac 480
132         tttcctcctg ccagagatgg acaactgccg ctcttcctcc agcccctacg tgtccaatgc 540
133         tgtgcagagg gacgcgccgc tcgaatacga tgactcggtg cagaggctgc aagtgctgga 600
134         gaacatcatg gaaaacaaca ctcagtggct aatgaagctt gagaattata tccaggacaa 660
135         catgaagaaa gaaatggtag agatacagca gaatgcagta cagaaccaga cggctgtgat 720
136         gatagaaata gggacaaacc tgttgaacca aacagctgag caaacgcgga agttaactga 780
137         tgtggaagcc caagtattaa atcagaccac gagacttgaa cttcagctct tggaacactc 840
138         cctctcgaca aacaaattgg aaaaacagat tttggaccag accagtgaaa taaacaaatt 900
139         gcaagataag aacagtttcc tagaaaagaa ggtgctagct atggaagaca agcacatcat 960
140         ccaactacag tcaataaaag aagagaaaga tcagctacag gtgttagtat ccaagcaaaa 1020
141         ttccatcatt gaagaactag aaaaaaaaat agtgactgcc acggtgaata attcagttct 1080
142         tcaaaagcag caacatgatc tcatggagac agttaataac ttactgacta tgatgtccac 1140
143         atcaaactca gctaaggacc ccactgttgc taaagaagaa caaatcagct tcagagactg 1200
144         tgctgaagta ttcaaatcag gacacaccac aaatggcatc tacacgttaa cattccctaa 1260
```

ttctacagaa gagatcaagg cctactgtga catggaagct ggaggaggcg ggtggacaat 1320
tattcagcga cgtgaggatg gcagcgttga ttttcagagg acttggaaag aatataaagt 1380
gggatttggt aacccttcag gagaatattg gctgggaaat gagtttgttt cgcaactgac 1440
taatcagcaa cgctatgtgc ttaaaataca ccttaaagac tgggaaggga atgaggctta 1500
ctcattgtat gaacatttct atctctcaag tgaagaactc aattatagga ttcaccttaa 1560
aggacttaca gggacagccg gcaaaataag cagcatcagc caaccaggaa atgattttag 1620
cacaaaggat ggagacaacg acaaatgtat ttgcaaatgt tcacaaatgc taacaggagg 1680
ctggtggttt gatgcatgtg gtccttccaa cttgaacgga atgtactatc cacagaggca 1740
gaacacaaat aagttcaacg gcattaaatg gtactactgg aaaggctcag gctattcgct 1800
caaggccaca accatgatga tccgaccagc agatttctaa acatcccagt ccacctgagg 1860
aactgtctcg aactattttc aaagacttaa gcccagtgca ctgaaagtca cggctgcgca 1920
ctgtgtcctc ttccaccaca gagggcgtgt gctcggtgct gacgggaccc acatgctcca 1980
gattagagcc tgtaaacttt atcacttaaa cttgcatcac ttaacggacc aaagcaagac 2040
cctaaacatc cataattgtg attagacaga acacctatgc aaagatgaac ccgaggctga 2100
gaatcagact gacagtttac agacgctgct gtcacaacca agaatgttat gtgcaagttt 2160
atcagtaaat aactggaaaa cagaacactt atgttataca atacagatca tcttggaact 2220
gcattcttct gagcactgtt tatacactgt gtaaataccc atatgtcct 2269

<210> SEQ ID NO 4
<211> LENGTH: 496
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 4

Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
1 5 10 15
Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
20 25 30
Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
35 40 45
Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
50 55 60
Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
65 70 75 80
Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
85 90 95
Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
100 105 110
Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
115 120 125
Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
130 135 140
Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
145 150 155 160
Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp
165 170 175
Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
180 185 190
Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
195 200 205
Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
210 215 220

```
195         Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn
196         225                 230                 235                 240
197         Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn
198                         245                 250                 255
199         Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ser Ala Lys Asp Pro Thr
200                     260                 265                 270
201         Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe
202                 275                 280                 285
203         Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn
204             290                 295                 300
205         Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly Gly
206         305                 310                 315                 320
207         Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln
208                         325                 330                 335
209         Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu
210                     340                 345                 350
211         Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg
212                 355                 360                 365
213         Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr
214             370                 375                 380
215         Ser Leu Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg
216         385                 390                 395                 400
217         Ile His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile
218                         405                 410                 415
219         Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys
220                     420                 425                 430
221         Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp
222                 435                 440                 445
223         Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln
224             450                 455                 460
225         Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser
226         465                 470                 475                 480
227         Gly Tyr Ser Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp Phe
228                         485                 490                 495
229   <210> SEQ ID NO 5
230   <211> LENGTH: 495
231   <212> TYPE: PRT
232   <213> ORGANISM: Homo sapiens
233   <400> SEQUENCE: 5
234         Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
235           1               5                  10                  15
236         Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
237                       20                  25                  30
238         Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
239                   35                  40                  45
240         Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
241                50                  55                  60
242         Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Phe Ser Ser Gln Lys Leu
243          65                  70                  75                  80
244         Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp Leu Gln Lys
```

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/351,149**

Input Set: **I351149.RAW**

Line	?	Error/Warning	Original Text